

T300X

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: COLOTTA, Francesco  
MUZIO, Marta  
MANTOVANI, Alberto
- (ii) TITLE OF INVENTION: INTERLEUKIN-1 ANTAGONIST, DNA ENCODING SAME,  
AND ANTIBODIES THERETO
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: BROWDY AND NEIMARK  
(B) STREET: 419 Seventh Street, N.W., Suite 300  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20004
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/476,860  
(B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: IT MI 94 A 002097  
(B) FILING DATE: 13-OCT-1994
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: YUN, Allen C.  
(B) REGISTRATION NUMBER: 37,971  
(C) REFERENCE/DOCKET NUMBER: COLOTTA=1A
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 202-628-5197  
(B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:  
(D) OTHER INFORMATION: RT-PCR oligonucleotide named IRA5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGACTTGTA TGAAGAAGGA GGTGG

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(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (D) OTHER INFORMATION: RT-PCR oligonucleotide corresponding to 60-79 of B-actin
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCGCTCGTCG TCGACAACGG

20

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (D) OTHER INFORMATION: RT-PCR backward oligonucleotide complementary to 430-449
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GATAGACAAC GTACATGGCT G

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(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 87 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (D) OTHER INFORMATION: Sequence of sIL-1ra not in common
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 24..86
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GAATTCCGGG CTGCAGTCAC AGA ATG GAA ATC TGC AGA GGC CTC CGC AGT  
Met Glu Ile Cys Arg Gly Leu Arg Ser  
1 5

50

CAC CTA ATC ACT CTC CTC CTC TTC CTG TTC CAT TCA G  
 His Leu Ile Thr Leu Leu Leu Phe Leu Phe His Ser  
 10 15 20

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(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu  
 1 5 10 15  
 Phe Leu Phe His Ser  
 20

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: Sequence of intracellular IL-1ra  
 typeI not in common

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 33..41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA G  
 Met Ala Leu  
 1

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(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: Sequence of intracellular IL-1ra  
typeII not in common

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 33..104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGAAGACCT	CCTGTCCTAT	GAGGCCCTCC	CC	ATG	GCT	TTA	GCT	GAC	TTG	TAT	53
				Met	Ala	Leu	Ala	Asp	Leu	Tyr	
				1				5			
GAA	GAA	GGA	GGT	GGA	GGA	GGA	GGA	GAA	GGT	GAA	101
Glu	Glu	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Gly	Glu	
		10				15				20	
AAG	G										105
Lys											

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Ala	Leu	Ala	Asp	Leu	Tyr	Glu	Glu	Gly	Gly	Gly	Gly	Glu
1				5					10				15
Gly	Glu	Asp	Asn	Ala	Asp	Ser	Lys						
			20										

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: Common IL-1ra sequence; a nucleotide G  
was added in the first position, for computer program  
reason, in order to encode the first amino acid Glu  
and further in order to avoid the creation of a stop  
codon in the inner region of the sequence

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAG	ACG	ATC	TGC	CGA	CCC	TCT	GGG	AGA	AAA	TCC	AGC	AAG	ATG	CAA	GCC	48
Glu	Thr	Ile	Cys	Arg	Pro	Ser	Gly	Arg	Lys	Ser	Ser	Lys	Met	Gln	Ala	
1				5					10					15		
TTC	AGA	ATC	TGG	GAT	GTT	AAC	CAG	AAG	ACC	TTC	TAT	CTG	AGG	AAC	AAC	96
Phe	Arg	Ile	Trp	Asp	Val	Asn	Gln	Lys	Thr	Phe	Tyr	Leu	Arg	Asn	Asn	
			20					25					30			
CAA	CTA	GTT	GCT	GGA	TAC	TTG	CAA	GGA	CCA	AAT	GTC	AAT	TTA	GAA	GAA	144
Gln	Leu	Val	Ala	Gly	Tyr	Leu	Gln	Gly	Pro	Asn	Val	Asn	Leu	Glu	Glu	
		35					40					45				
AAG	ATA	GAT	GTG	GTA	CCC	ATT	GAG	CCT	CAT	GCT	CTG	TTC	TTG	GGA	ATC	192
Lys	Ile	Asp	Val	Val	Pro	Ile	Glu	Pro	His	Ala	Leu	Phe	Leu	Gly	Ile	
	50					55					60					
CAT	GGA	GGG	AAG	ATG	TGC	CTG	TCC	TGT	GTC	AAG	TCT	GGT	GAT	GAG	ACC	240
His	Gly	Gly	Lys	Met	Cys	Leu	Ser	Cys	Val	Lys	Ser	Gly	Asp	Glu	Thr	
65					70					75				80		
AGA	CTC	CAG	CTG	GAG	GCA	GTT	AAC	ATC	ACT	GAC	CTG	AGC	GAG	AAC	AGA	288
Arg	Leu	Gln	Leu	Glu	Ala	Val	Asn	Ile	Thr	Asp	Leu	Ser	Glu	Asn	Arg	
				85					90					95		
AAG	CAG	GAC	AAG	CGC	TTC	GCC	TTC	ATC	CGC	TCA	GAC	AGT	GGC	CCC	ACC	336
Lys	Gln	Asp	Lys	Arg	Phe	Ala	Phe	Ile	Arg	Ser	Asp	Ser	Gly	Pro	Thr	
			100				105						110			
ACC	AGT	TTT	GAG	TCT	GCC	GCC	TGC	CCC	GGT	TGG	TTC	CTC	TGC	ACA	GCG	384
Thr	Ser	Phe	Glu	Ser	Ala	Ala	Cys	Pro	Gly	Trp	Phe	Leu	Cys	Thr	Ala	
		115					120					125				
ATG	GAA	GCT	GAC	CAG	CCC	GTC	AGC	CTC	ACC	AAT	ATG	CCT	GAC	GAA	GGC	432
Met	Glu	Ala	Asp	Gln	Pro	Val	Ser	Leu	Thr	Asn	Met	Pro	Asp	Glu	Gly	
	130					135					140					
GTC	ATG	GTC	ACC	AAA	TTC	TAC	TTC	CAG	GAG	GAC	GAG	TAGTAC				474
Val	Met	Val	Thr	Lys	Phe	Tyr	Phe	Gln	Glu	Asp	Glu					
145					150					155						

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 156 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Glu	Thr	Ile	Cys	Arg	Pro	Ser	Gly	Arg	Lys	Ser	Ser	Lys	Met	Gln	Ala
1				5					10					15	
Phe	Arg	Ile	Trp	Asp	Val	Asn	Gln	Lys	Thr	Phe	Tyr	Leu	Arg	Asn	Asn
			20					25					30		
Gln	Leu	Val	Ala	Gly	Tyr	Leu	Gln	Gly	Pro	Asn	Val	Asn	Leu	Glu	Glu
		35					40					45			

Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile  
 50 55 60  
 His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr  
 65 70 75 80  
 Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg  
 85 90 95  
 Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr  
 100 105 110  
 Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala  
 115 120 125  
 Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly  
 130 135 140  
 Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp Glu  
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
  - (D) OTHER INFORMATION: A portion of the intracellular IL-1ra typeII not in common
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 

Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu Gly Glu Asp  
 1 5 10 15  
 Asn Ala Asp Ser Lys  
 20

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (D) OTHER INFORMATION: Intracellular IL-1ra typeII

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 34..573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CAGAAGGACC TCCTGTCCTA TGAGGCCCTC CCC ATG GCT TTA GCT GAC TTG TAT	54
Met Ala Leu Ala Asp Leu Tyr	
1 5	
GAA GAA GGA GGT GGA GGA GGA GGA GAA GGT GAA GAC AAT GCT GAC TCA	102
Glu Glu Gly Gly Gly Gly Gly Gly Glu Gly Glu Asp Asn Ala Asp Ser	
10 15 20	
AAG GAG ACG ATC TGC CGA CCC TCT GGG AGA AAA TCC AGC AAG ATG CAA	150
Lys Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln	
25 30 35	
GCC TTC AGA ATC TGG GAT GTT AAC CAG AAG ACC TTC TAT CTG AGG AAC	198
Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn	
40 45 50 55	
AAC CAA CTA GTT GCT GGA TAC TTG CAA GGA CCA AAT GTC AAT TTA GAA	246
Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu	
60 65 70	
GAA AAG ATA GAT GTG GTA CCC ATT GAG CCT CAT GCT CTG TTC TTG GGA	294
Glu Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly	
75 80 85	
ATC CAT GGA GGG AAG ATG TGC CTG TCC TGT GTC AAG TCT GGT GAT GAG	342
Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu	
90 95 100	
ACC AGA CTC CAG CTG GAG GCA GTT AAC ATC ACT GAC CTG AGC GAG AAC	390
Thr Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn	
105 110 115	
AGA AAG CAG GAC AAG CGC TTC GCC TTC ATC CGC TCA GAC AGT GGC CCC	438
Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro	
120 125 130 135	
ACC ACC AGT TTT GAG TCT GCC GCC TGC CCC GGT TGG TTC CTC TGC ACA	486
Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr	
140 145 150	
GCG ATG GAA GCT GAC CAG CCC GTC AGC CTC ACC AAT ATG CCT GAC GAA	534
Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu	
155 160 165	
GGC GTC ATG GTC ACC AAA TTC TAC TTC CAG GAG GAC GAG TAGTAC	579
Gly Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp Glu	
170 175 180	

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Ala Leu Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu  
1 5 10 15  
Gly Glu Asp Asn Ala Asp Ser Lys Glu Thr Ile Cys Arg Pro Ser Gly  
20 25 30  
Arg Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln  
35 40 45  
Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln  
50 55 60  
Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu  
65 70 75 80  
Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser  
85 90 95  
Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn  
100 105 110  
Ile Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe  
115 120 125  
Ile Arg Ser Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys  
130 135 140  
Pro Gly Trp Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser  
145 150 155 160  
Leu Thr Asn Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe  
165 170 175  
Gln Glu Asp Glu  
180

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTGAGTCAG CATTGTCTTC A

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGACTTGTA TGAAGAAGGA GGTGG

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(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu Gly Glu Asp  
1 5 10 15

Asn Ala Asp Ser Lys  
20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3176 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CCATGGCTTT AGGTAAGCTC CTTCCACTCT 60  
CATTTTTTTCA CCTGAGAAAT GAGAGAGGAA AATGTCTACA ATTGGTGT TT ATCAAATGCT 120  
TTCAGGCTCT GGTGAGCAAG CGTCCAGGAA AATGTCAAGC GCATGGAGCT CCAGGCCTGT 180  
CTGGGGGATC TGGGCACGGG GAGGCATCCA TGGGAGACCA TGCAGGCACT CTGAGGCAGG 240  
GGCTGCAAGC TAGTGCCTGC TGGGGCAGCA GGTGAACAGA GAGGTGTAAC TGCTGTGACA 300  
GAAGTCATGG AGTCCTTGGA GTGTGAGGGT CATT TTCCAC TGTGATAGA ATAGGGAAAT 360  
TGGTGAAATA GCCCTGT TAA ATGAGAGAAA GAACAGTGTG AGCTCAATGA GAAATACTAA 420  
TAGAATGTGG CACTGAGCCA CAAGGTCTGA GGGTTGATTG ATAAGGAAGG GTGGGGACTG 480  
TGGAGAATTA AGGGCTTGGC ACAGGTCAGT TCCACCAGTT GTCACAAGAG AATGCAGGCT 540  
CAGGTGGCCA GAACTTCTCG CTTTTCCAGA AGAGTCCGAT ATTCTGATTT CATTATATAT 600  
AGTATTCTGA TTAAACCAGA CAATAAAGCA AGCAGATAAA ATATTTAAAG TATAAGCTGC 660  
CAGTTTGCAA CCTCCGGTTA GGATTTGTGT GGGGCAAAGA AAAAACTCT CAGGATCATT 720  
GGTATGTAGA CTCTAATTTT AAGTTTCTAA TTTAAATTG GCCCTGAGG CTGGGCGTGG 780  
TGGCTCACAC CTGTAATCCC AGCATTTTGG GAGGCCAAGG TGGGTGGATC TCTTGAGGTC 840

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AGTTACTCTA	TGAGATAGGA	GTTCAGCCCA	AAAGAAACAC	CATAAGAACA	AATATAATTC	2820
TTGCTTATGT	TAACCATGCA	ATGAAGCAGA	GAGAAAAAGT	CAGTGGCCTC	TTTAGGAGGA	2880
CTGTAGTGTG	GGAAGAAATA	ACTAAACTGG	GTTTCAATCC	TGGCCTGGCC	AGGATCTGGA	2940
GCAAGTGAGT	TAATCTTTCA	AAGCCTTGAG	TAGTTTATAA	AAGAATGGCC	ACTCCATAGA	3000
CAGAGTAGCC	TGAACCTTGA	GTTCTTCTAT	AAAGTCACTA	TGAATTTATA	CTCATTTTGA	3060
AAGTGGGTGT	CAATATGTCT	GTCCACTTTG	CACAGCTGTT	ATGTGGACAA	AAGGAGATCT	3120
GTGTGAAAGT	GTAACACAGA	GCCTAAACTA	TAACAGGTAA	GCAACACAGT	TGTCCC	3176